forest management note

Note 46 Northwest Region

JACK PINE FAMILY SELECTION IN SASKATCHEWAN BASED ON 10-YEAR MEASUREMENT

INTRODUCTION

Forestry Canada began a program of genetic improvement of jack pine (*Pinus banksiana* Lamb.) in three areas in the prairie provinces in 1967. The main objective was to provide genetically improved seed, seedlings, scions, and grafts to cooperating agencies for seed orchard establishment. Genetic improvement is pursued by selection within breeding populations consisting of grafts of selected wild parent trees and their open-pollinated progenies, based on analysis of measurements from replicated family-test plantations. Genetic improvement is also pursued by selection of source stands according to the average family-test performance of their progenies.

Benefits of genetic improvement are fully realized only after seed orchards are established from the selected trees and cone crops of useful size are produced in the seed orchards. It is important to identify the selected trees and to document the available gains as soon as possible after analysis of measurements indicates that useful genetic gain can be captured, to support seed orchard establishment by cooperators. Gains available from selection at 10 years from planting have been reported for the eastern breeding district, located in southeastern Manitoba (Klein 1983). This report presents selection results for the western breeding district, which covers the southern portion of the forest zone in central Saskatchewan to eastern Alberta (Fig. 1).

METHODS

Test families were chosen from 254 parent-tree seed lots that were collected in the fall of 1968, 1969, and 1971. Selection criteria for seed parents were superior bole quality (no forks, minimal crook and flat branching habit), and good vigor. Following felling, scions (branch cuttings) and open-pollinated cones were collected from the parent trees, and seed was extracted. Grafts produced from the scions are genetically identical to the tree from which they were collected, while seeds extracted from the cones of any one tree are presumed to have been pollinated by several pollen parents. Grafts of the majority of families tested are growing in a clone bank near Wildwood, Alberta, and seed from the parent trees is stored at the Northern Forestry Centre. Obtaining a good source distribution was the initial basis for choosing test families from among the progenies. Some modifications to the original choice were made based on seedling survival.

Four family-test plantations were established in 1974 with 214 open-pollinated families and two control lots. Seed for the two control lots was obtained by making stand collections within 50 km of the test plantation locations. Stock was grown in 0.35-L Spencer-Lemaire "Tinus" Rootrainers. Each plantation had three replications each containing one four-tree plot of each of the 216 family and control lots. Two locations about 200 km apart were chosen for the plantations, and two plantations were established in each location, separated by a few kilometres. Forty-eight trees from each family were planted for a total of 10 368 trees in the entire test. Trees were planted at 2.5×2.5 m spacing in furrows created by finned barrels and anchor chains. Source stands for the test families and control lots, as well as the test plantation locations, are shown in Figure 2.

Height was recorded prior to planting and again at age 5. The 10-year measurement was carried out in the

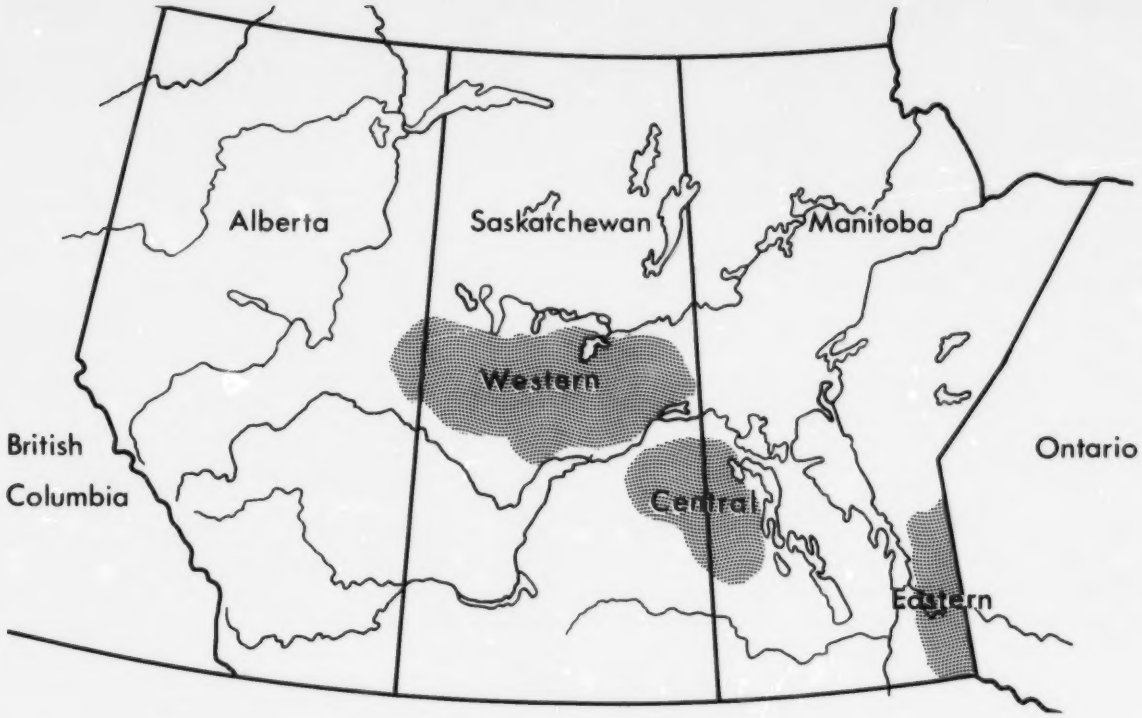

Figure 1. Breeding district boundaries.

fall of 1983, at which time height, diameter outside bark at 1.3 m above ground, and a subjective grade for stem quality rated on a scale of 1 (best) to 5 (poorest) relative to adjacent trees were recorded. A good grade was assigned to a tree if it was relatively straight and free of forks, with nearly horizontal branches, and if it showed fast recovery of apical dominance after loss of the original leader. Trees with severe crooks or many moderate crooks, persistent forks resulting from delayed recovery of dominant apical growth or acute branch angle had correspondingly poor quality grades.

Mean values were calculated for each family and control lot, and for the entire test. In order to rank families for selection the deviation of the family means from the test means for height, diameter and stem quality had to be combined into a single value. The formula that best combines values for several traits is a selection index, which is constructed by solving a set of equations using relative economic weights, trait variances, and intertrait covariances (Baker 1986). For the western district family test the optimum selection index was:

$$S_i = H_i + 0.685\ D_i - 9.5\ Q_i$$

where S_i = selection index score for family i,
H_i = deviation in cm of the mean height of family i from the test mean,
D_i = deviation in mm of the mean diameter of family i from the test mean, and
Q_i = the deviation of the mean quality of family i from the test mean.

Family scores were calculated by substituting their family mean deviation for the three traits into the selection index. The families were ranked from 1 to 216 based on their scores.

For the purpose of determining volume differences between families or groups of families and because there are no volume tables for trees only 10 years old, an index of relative volume was created as the product of the height and the square of half the diameter at 1.3 m. This index treats the stem as a cone and underestimates actual volume by not allowing for the taper between the butt and 1.3 m, but should provide a valid indication of relative volume for comparisons among families.

RESULTS AND DISCUSSION

Parent tree origin and family means for the 40 best-ranked families are presented in Table 1, with the group means for the top 40 families, the control lots, and the test means.

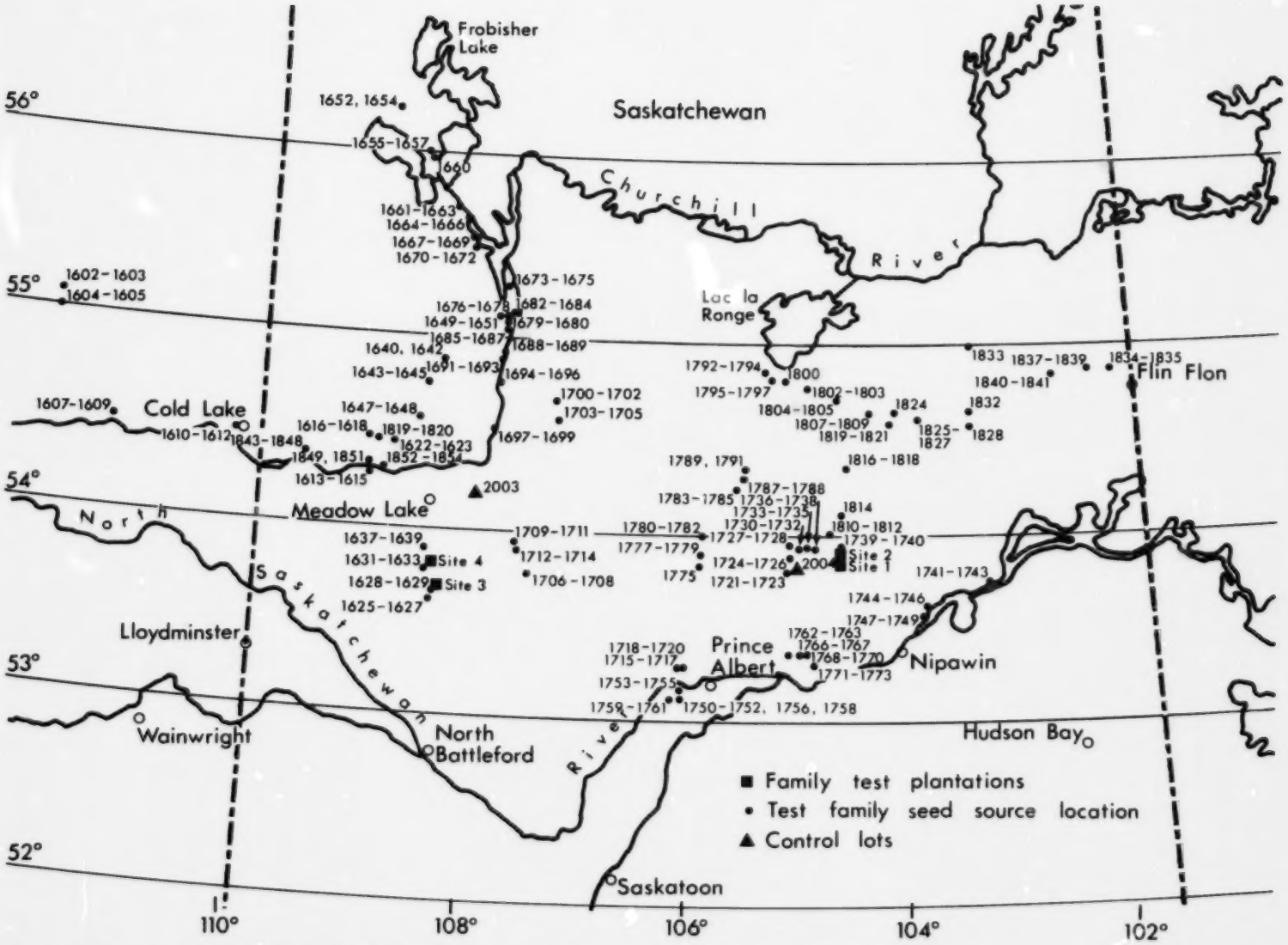

Figure 2. Western breeding district family test seed sources.

Table 1. Performance values for selected families in the western district family test

Rank	Family	Latitude (°)	Longitude (°)	Elevation (m)	Mean at age 10 years: Height (cm)	Diameter (cm)	Quality	Volume index[a] (cm^3)	Score[b]
1	1707	53.75	107.50	460	333.7	4.73	2.29	1866	38.8
2	1775	53.80	105.92	550	328.3	4.82	2.37	1904	33.3
3	1718	53.25	106.05	460	324.4	4.42	2.31	1582	27.1
4	1773	53.28	104.87	460	328.1	4.43	2.86	1609	25.8
5	1719	53.25	106.08	460	327.4	4.20	2.62	1442	25.7
6	1623	54.43	108.77	510	324.9	4.33	2.49	1521	25.4
7	1752	53.08	106.08	460	324.8	4.35	2.53	1537	25.0
8	1812	53.97	104.75	520	322.9	4.50	2.48	1633	24.7
9	1669	55.55	108.08	430	324.9	4.20	2.49	1431	24.5
10	1628	53.62	108.35	730	321.6	4.32	2.24	1502	24.4
11	1759	53.08	106.17	460	328.3	4.25	2.91	1482	24.3
12	1618	54.43	109.00	500	322.2	4.47	2.43	1608	24.2
13	1608	54.45	111.40	690	321.8	4.26	2.34	1458	23.2
14	1769	53.33	104.93	460	324.3	4.42	2.79	1582	22.5
15	1854	54.28	108.85	520	321.1	4.35	2.52	1518	21.5
16	1613	54.25	109.00	470	319.5	4.31	2.46	1481	20.2
17	1768	53.33	104.93	460	318.8	4.55	2.56	1653	20.2
18	1771	53.28	104.87	460	321.0	4.27	2.61	1460	19.9
19	1825	54.58	103.97	370	320.1	4.38	2.60	1537	19.8
20	1637	53.87	108.43	730	317.2	4.24	2.22	1427	19.7
21	1772	53.28	104.87	460	321.2	4.32	2.70	1501	19.7
22	1789	54.32	105.52	520	315.9	4.40	2.23	1530	19.4
23	1614	54.25	109.00	470	320.0	4.19	2.52	1404	19.2
24	1743	53.72	103.27	310	318.8	4.45	2.60	1578	19.1
25	1770	53.33	104.93	460	321.7	4.27	2.82	1465	18.7
26	1737	53.92	104.87	550	316.9	4.43	2.46	1558	18.4
27	1748	53.53	103.80	340	320.0	4.28	2.73	1467	17.9
28	1844	54.33	109.62	560	320.7	4.52	2.97	1637	17.9
29	1779	53.87	105.93	580	317.0	4.49	2.58	1598	17.7
30	1753	53.13	106.08	460	321.8	4.23	2.90	1436	17.6
31	1694	54.75	107.82	460	319.5	4.38	2.88	1536	16.7
32	1615	54.25	109.00	470	318.2	4.09	2.57	1328	16.3
33	1717	53.25	106.12	460	318.1	4.38	2.78	1525	16.2
34	1746	53.60	103.73	340	316.3	4.20	2.46	1392	16.2
35	1706	53.75	107.50	460	314.5	4.48	2.54	1580	15.5
36	1639	53.87	108.43	730	316.6	4.39	2.70	1527	15.5
37	1709	53.90	107.62	560	314.3	4.28	2.39	1441	15.3
38	1705	54.55	107.27	490	315.2	4.53	2.73	1616	14.8
39	1756	53.08	106.08	460	315.7	4.06	2.46	1301	14.6
40	1754	53.13	106.08	460	317.0	4.26	2.84	1438	13.6
Mean of best 40 families					320.9	4.36	2.57	1527	
Mean of control families					299.2	3.95	2.84	1167	
Mean of all families					304.1	4.05	2.77	1256	

[a] Because no volume tables for 10-year old trees exist, an index of relative volume was created as the product of the height and the square of the radius at 1.3 m.

[b] Score is calculated by substituting family mean values into selection index.

Mean values for the family test at 10 years were 304.1 cm for height, 4.05 cm for diameter and 2.77 for quality. Analysis of variance detected significant differences among families for height, diameter, and stem quality at age 10.

Jack pine planting stock currently being produced in Saskatchewan is grown from wild seed extracted from cones collected from squirrel caches. No selection is applied to the parent trees. The two control lots tested were drawn from bulked stand collections made without parent tree selection and are likely representative of the seed presently used in seedling production. Mean height, diameter, and quality for the test was about 2% better than that of the control lots, indicating that the test families were, on average, genetically as good as, or better than, the wild population. Calculations of genetic gains that follow will be compared against the test mean since it comes from a broader geographic base and gives a more conservative estimate of improvement.

The 40 top scoring families were identified as the most suitable for use in seed orchard establishment. For these selected trees the mean height was 320.9 cm, the mean diameter was 4.36 cm, and the mean quality was 2.57. The difference between the selected-family mean and the test mean is the selection differential for that trait. Selection differentials for this test were 16.8 cm (5.5%) for height, 0.31 cm (7.7%) for diameter, and −0.20 (7.2%) for stem quality.

A portion of the selection differential for each trait is due to nongenetic effects on the trees. The portion due to genetic differences (heritability) can be estimated from genetic and phenotypic variances calculated by analysis of variance (Zobel and Talbert 1984). Heritability of family selection was calculated to be 0.65 for height, 0.52 for diameter, and 0.48 for stem quality.

The product of the heritability and the selection differential is the expected gain from family selection for that trait. This gain is the average improvement (at age 10) that would be achieved by using average individual trees of the selected families as parents in a seed orchard. There would be no difference in gain expected by using either grafts of average progeny trees or seed from controlled pollination between average individual trees of the selected progenies. At age 10, trees from such a seed orchard would have an expected improvement of 3.6% for height, 4.0% for diameter, and 3.3% for stem quality over the test mean. At 10 years the stem volume of these trees (estimated to be the product of the mean height and the square of the mean radius) would be 11% greater than the test mean.

Greater genetic gains are possible by establishing a seed orchard with seed parent grafts or with selected individuals within the selected families. Seed parent grafts of the best families are genetically superior to their average progeny since the latter achieved superiority despite being pollinated by near-average pollen parents. In selected families lacking parent grafts, progeny trees with the best individual score should be genetically above-average for their family. The genetic superiority of selected progeny trees over their family test mean may be about 40% of their family superiority over the test mean (Klein 1986). Seed parent grafts of selected families are probably superior to even the best of their progeny. The use of grafts or control-pollinated seedlings, produced from seed-parent grafts and selected progeny trees, in seed orchard establishment should raise the expected gain by about 50%, resulting in an improvement of 16.5% for volume and 5.1% for quality.

During parent tree selection up to three trees per stand were collected, and often several stands 5–10 km apart were sampled, allowing test means for several families to be geographically grouped to select existing sources of more productive trees for operational seed collection. One hundred and seventy-one families were grouped on the basis of geographic proximity into 13 source areas. Forty-three test families could not be put in any group due to relative isolation. The source areas contained from 6 to 24 test families, and were each assigned a group score which was the mean of the scores of all the families that originated within it. Source area boundaries are shown in Figure 3 along with the group score. Areas are identified by their score rank. The two areas with the best scores are located within 50 km of Prince Albert, near the confluence of the Saskatchewan and North Saskatchewan rivers. These stands have a combined mean volume of 1366.6 cm^3 and a quality of 2.72 based on 25 family means; this is an 8.8% volume increase and a 1.8% better quality than the test mean. A third source of existing seed wth a high score is located northwest of Meadow Lake. The mean volume of 23 families in that area was 7.1% higher than the test mean with a marginal improvement in quality. These gains may be realized immediately by collecting open-pollinated seed from natural jack pine populations in these three areas. Information on the three selected source areas is presented in Table 2.

CONCLUSIONS

Forest managers in the western breeding district can take several steps to improve the genetic composition and value of jack pine planting stock. Immediate increases in

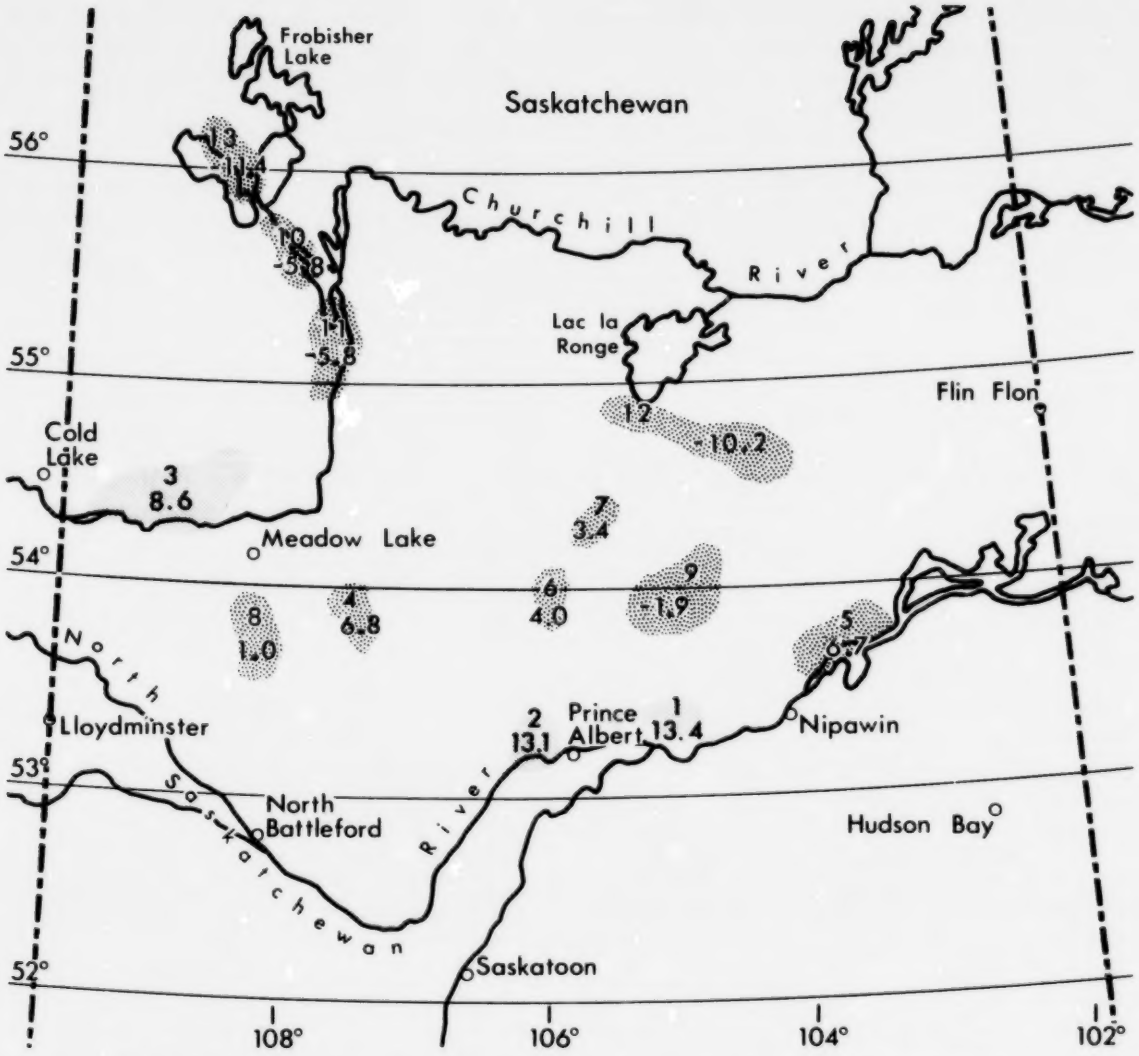

Figure 3. Multiple family source areas. Numbers within area boundary are area rank over area score.

Table 2. Superior wild seed source areas

Area rank	Description	Number of families	Mean height (cm)	Mean diameter (cm)	Mean volume index (cm^3)	Mean quality	Area mean score
1	Prince Albert (east)	10	315.9	4.19	1394.1	2.70	13.4
2	Prince Albert (west)	15	316.4	4.12	1348.2	2.74	13.1
3	Meadow Lake	23	311.8	4.15	1344.7	2.75	8.6

10 year volume of 8.8% could be realized by collecting seed from two areas identified as superior general seed collection areas. The output from a seed orchard established with average trees of the selected families as parent stock would have an expected improvement of 11% for volume and 3.3% for quality at ten years of age. Since parent clones exist for most selected families, it makes sense to establish any seed orchard with grafts of selected parent clones or seed from controlled mating of selected parent clones. For families lacking parent clones the progeny test trees with the best individual score should be substituted. Output from such a seed orchard should have an expected improvement over unimproved seed of 16.5% for volume and 5.1% for quality.

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